



SEQUENCE LISTING

<110> Clausen, Henrik

<120> UDP-N-Acetylglucosamine:
Galactose-beta-1,3-N-Acetylgalactosamine-alpha-R /
N-Acetylglucosamine-beta-1,3-N-Acetylgalactosamine-alpha-R (GlcNAc to GalNAc)
beta-1,6-N-Acetylglucosaminyltransferase, C2/4

<130> P199801704 WO JNY

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<150> DK PA 1998 01605

<151> 1998-12-04

<160> 10 ✓

<170> PatentIn Ver. 2.1

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<211> 2319

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (496)..(1809)

<223> cDNA sequence

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tcccattctg	tgacg	atg	gtt	caa	tgg	aag	aga	ctc	tgc	cag	ctg	cat	tac	531		
		Met	Val	Gln	Trp	Lys	Arg	Leu	Cys	Gln	Leu	His	Tyr			
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ttg	tgg	gct	ctg	ggc	tgc	tat	atg	ctg	ctg	gcc	act	gtg	gct	ctg	aaa	579
Leu	Trp	Ala	Leu	Gly	Cys	Tyr	Met	Leu	Leu	Ala	Thr	Val	Ala	Leu	Lys	
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ctt	tct	ttc	agg	ttg	aag	tgt	gac	tct	gac	cac	ttg	ggt	ctg	gag	tcc	627
Leu	Ser	Phe	Arg	Leu	Lys	Cys	Asp	Ser	Asp	His	Leu	Gly	Leu	Glu	Ser	
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agg	gaa	tct	caa	agc	cag	tac	tgt	agg	aat	atc	ttg	tat	aat	ttc	ctg	675
Arg	Glu	Ser	Gln	Ser	Gln	Tyr	Cys	Arg	Asn	Ile	Leu	Tyr	Asn	Phe	Leu	
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aaa	ctt	cca	gca	aag	agg	tct	atc	aac	tgt	tca	ggg	gtc	acc	cga	ggg	723
Lys	Leu	Pro	Ala	Lys	Arg	Ser	Ile	Asn	Cys	Ser	Gly	Val	Thr	Arg	Gly	
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gac	caa	gag	gca	gtg	ctt	cag	gct	att	ctg	aat	aac	ctg	gag	gtc	aag	771
Asp	Gln	Glu	Ala	Val	Leu	Gln	Ala	Ile	Leu	Asn	Asn	Leu	Glu	Val	Lys	
			80					85					90			
aag	aag	cga	gag	cct	ttc	aca	gac	acc	cac	tac	ctc	tcc	ctc	acc	aga	819
Lys	Lys	Arg	Glu	Pro	Phe	Thr	Asp	Thr	His	Tyr	Leu	Ser	Leu	Thr	Arg	
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gac	tgt	gag	cac	ttc	aag	gct	gaa	agg	aag	ttc	ata	cag	ttc	cca	ctg	867
Asp	Cys	Glu	His	Phe	Lys	Ala	Glu	Arg	Lys	Phe	Ile	Gln	Phe	Pro	Leu	
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agc	aaa	gaa	gag	gtg	gag	ttc	cct	att	gca	tac	tct	atg	gtg	att	cat	915
Ser	Lys	Glu	Glu	Val	Glu	Phe	Pro	Ile	Ala	Tyr	Ser	Met	Val	Ile	His	
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Glu	Lys	Ile	Glu	Asn	Phe	Glu	Arg	Leu	Leu	Arg	Ala	Val	Tyr	Ala	Pro	
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cag	aac	ata	tac	tgt	gtc	cat	gtg	gat	gag	aag	tcc	cca	gaa	act	ttc	1011
Gln	Asn	Ile	Tyr	Cys	Val	His	Val	Asp	Glu	Lys	Ser	Pro	Glu	Thr	Phe	
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aaa	gag	gcg	gtc	aaa	gca	att	att	tct	tgc	ttc	cca	aat	gtc	ttc	ata	1059
Lys	Glu	Ala	Val	Lys	Ala	Ile	Ile	Ser	Cys	Phe	Pro	Asn	Val	Phe	Ile	
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gcc	agt	aag	ctg	gtt	cgg	gtg	gtt	tat	gcc	tcc	tgg	tcc	agg	gtg	caa	1107
Ala	Ser	Lys	Leu	Val	Arg	Val	Val	Tyr	Ala	Ser	Trp	Ser	Arg	Val	Gln	

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gct gac ctc aac tgc atg gaa gac ttg ctc cag agc tca gtg ccg tgg			1155
Ala Asp Leu Asn Cys Met Glu Asp Leu Leu Gln Ser Ser Val Pro Trp			
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aaa tac ttc ctg aat aca tgt ggg acg gac ttt cct ata aag agc aat			1203
Lys Tyr Phe Leu Asn Thr Cys Gly Thr Asp Phe Pro Ile Lys Ser Asn			
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gca gag atg gtc cag gct ctc aag atg ttg aat ggg agg aat agc atg			1251
Ala Glu Met Val Gln Ala Leu Lys Met Leu Asn Gly Arg Asn Ser Met			
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gag tca gag gta cct cct aag cac aaa gaa acc cgc tgg aaa tat cac			1299
Glu Ser Glu Val Pro Pro Lys His Lys Glu Thr Arg Trp Lys Tyr His			
	255	260	265
ttt gag gta gtg aga gac aca tta cac cta acc aac aag aag aag gat			1347
Phe Glu Val Val Arg Asp Thr Leu His Leu Thr Asn Lys Lys Lys Asp			
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cct ccc cct tat aat tta act atg ttt aca ggg aat gcg tac att gtg			1395
Pro Pro Pro Tyr Asn Leu Thr Met Phe Thr Gly Asn Ala Tyr Ile Val			
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gct tcc cga gat ttc gtc caa cat gtt ttg aag aac cct aaa tcc caa			1443
Ala Ser Arg Asp Phe Val Gln His Val Leu Lys Asn Pro Lys Ser Gln			
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caa ctg att gaa tgg gta aaa gac act tat agc cca gat gaa cac ctc			1491
Gln Leu Ile Glu Trp Val Lys Asp Thr Tyr Ser Pro Asp Glu His Leu			
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tgg gcc acc ctt cag cgt gca cgg tgg atg cct ggc tct gtt ccc aac			1539
Trp Ala Thr Leu Gln Arg Ala Arg Trp Met Pro Gly Ser Val Pro Asn			
	335	340	345
cac ccc aag tac gac atc tca gac atg act tct att gcc agg ctg gtc			1587
His Pro Lys Tyr Asp Ile Ser Asp Met Thr Ser Ile Ala Arg Leu Val			
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aag tgg cag ggt cat gag gga gac atc gat aag ggt gct cct tat gct			1635
Lys Trp Gln Gly His Glu Gly Asp Ile Asp Lys Gly Ala Pro Tyr Ala			
365	370	375	380
ccc tgc tct gga atc cac cag cgg gct atc tgc gtt tat ggg gct ggg			1683
Pro Cys Ser Gly Ile His Gln Arg Ala Ile Cys Val Tyr Gly Ala Gly			
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gac ttg aat tgg atg ctt caa aac cat cac ctg ttg gcc aac aag ttt 1731
 Asp Leu Asn Trp Met Leu Gln Asn His His Leu Leu Ala Asn Lys Phe
 400 405 410

gac cca aag gta gat gat aat gct ctt cag tgc tta gaa gaa tac cta 1779
 Asp Pro Lys Val Asp Asp Asn Ala Leu Gln Cys Leu Glu Glu Tyr Leu
 415 420 425

cgt tat aag gcc atc tat ggg act gaa ctt tgagacacac tatgagagcg 1829
 Arg Tyr Lys Ala Ile Tyr Gly Thr Glu Leu
 430 435

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 Leu Lys Cys Asp Ser Asp His Leu Gly Leu Glu Ser Arg Glu Ser Gln
 35 40 45
 Ser Gln Tyr Cys Arg Asn Ile Leu Tyr Asn Phe Leu Lys Leu Pro Ala
 50 55 60
 Lys Arg Ser Ile Asn Cys Ser Gly Val Thr Arg Gly Asp Gln Glu Ala

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Val	Leu	Gln	Ala	Ile	Leu	Asn	Asn	Leu	Glu	Val	Lys	Lys	Lys	Arg	Glu			
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Pro	Phe	Thr	Asp	Thr	His	Tyr	Leu	Ser	Leu	Thr	Arg	Asp	Cys	Glu	His			
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Phe	Lys	Ala	Glu	Arg	Lys	Phe	Ile	Gln	Phe	Pro	Leu	Ser	Lys	Glu	Glu			
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Val	Glu	Phe	Pro	Ile	Ala	Tyr	Ser	Met	Val	Ile	His	Glu	Lys	Ile	Glu			
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Asn	Phe	Glu	Arg	Leu	Leu	Arg	Ala	Val	Tyr	Ala	Pro	Gln	Asn	Ile	Tyr			
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Cys	Val	His	Val	Asp	Glu	Lys	Ser	Pro	Glu	Thr	Phe	Lys	Glu	Ala	Val			
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Lys	Ala	Ile	Ile	Ser	Cys	Phe	Pro	Asn	Val	Phe	Ile	Ala	Ser	Lys	Leu			
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Val	Arg	Val	Val	Tyr	Ala	Ser	Trp	Ser	Arg	Val	Gln	Ala	Asp	Leu	Asn			
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Gln	Ala	Leu	Lys	Met	Leu	Asn	Gly	Arg	Asn	Ser	Met	Glu	Ser	Glu	Val			
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Pro	Pro	Lys	His	Lys	Glu	Thr	Arg	Trp	Lys	Tyr	His	Phe	Glu	Val	Val			
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Arg	Asp	Thr	Leu	His	Leu	Thr	Asn	Lys	Lys	Lys	Asp	Pro	Pro	Pro	Tyr			
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Asn	Leu	Thr	Met	Phe	Thr	Gly	Asn	Ala	Tyr	Ile	Val	Ala	Ser	Arg	Asp			
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Phe	Val	Gln	His	Val	Leu	Lys	Asn	Pro	Lys	Ser	Gln	Gln	Leu	Ile	Glu			
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Trp	Val	Lys	Asp	Thr	Tyr	Ser	Pro	Asp	Glu	His	Leu	Trp	Ala	Thr	Leu			
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Gln Arg Ala Arg Trp Met Pro Gly Ser Val Pro Asn His Pro Lys Tyr
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 Asp Ile Ser Asp Met Thr Ser Ile Ala Arg Leu Val Lys Trp Gln Gly
 355 360 365
 His Glu Gly Asp Ile Asp Lys Gly Ala Pro Tyr Ala Pro Cys Ser Gly
 370 375 380
 Ile His Gln Arg Ala Ile Cys Val Tyr Gly Ala Gly Asp Leu Asn Trp
 385 390 395 400
 Met Leu Gln Asn His His Leu Leu Ala Asn Lys Phe Asp Pro Lys Val
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